SEQUENCE LISTING

<110> HALKIER, Torben
HAANING, Jesper

<120> Method for Down-Regulating Osteoprotegerin Ligand Activity

<130> 3631-0114P

<140> US 09/396,937
<141> 1999-09-15

<160> 36

<170> PatentIn Ver. 2.1

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cgcc atg cgc cgc gcc agc aga gac tac acc aag tac ctg cgt ggc tcg 229
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atg ttc gtg gcc ctc ctg ggg ctg ggg ctg ggc cag gtt gtc tgc agc 373
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gtt aat cag gat ggc ttt tat tac ctg tat gcc aac att tgc ttt cga   853
Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg
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cat cat gaa act tca gga gac cta gct aca gag tat ctt caa cta atg   901
His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met
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Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu
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Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
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         35                  40                  45
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 65                  70                  75                  80
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Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
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Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
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Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
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Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
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Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
        195                 200                 205
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
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His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
225                 230                 235                 240
Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
                245                 250                 255
Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe
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Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu
        275                 280                 285
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gcg cct tct gca ccg gct ccg gcg ccg cca ccc gcc gcc tcc cgc tcc   144
Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser
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                 85                  90                  95
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gac tcc tgc agg agg atg aaa caa gcc ttt cag ggg gcc gtg cag aag   384
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gaa ctg caa cac att gtg ggg cca cag cgc ttc tca gga gct cca gct   432
Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
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atg atg gaa ggc tca tgg ttg gat gtg gcc cag cga ggc aag cct gag   480
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145                 150                 155                 160
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Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
            180                 185                 190
gcc aag atc tct aac atg acg tta agc aac gga aaa cta agg gtt aac   624
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225                 230                 235                 240
gtc gtt aaa acc agc atc aaa atc cca agt tct cat aac ctg atg aaa   768
Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
                245                 250                 255
gga ggg agc acg aaa aac tgg tcg ggc aat tct gaa ttc cac ttt tat   816
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Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
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agc att cag gtg tcc aac cct tcc ctg ctg gat ccg gat caa gat gcg   912
Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
    290                 295                 300
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 65                  70                  75                  80
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                 85                  90                  95
Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
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Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
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Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
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Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
145                 150                 155                 160
Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
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Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
            180                 185                 190
Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
        195                 200                 205
Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
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Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
225                 230                 235                 240
Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
                245                 250                 255
Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
            260                 265                 270
Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
        275                 280                 285
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gggagagaac gatcgcggag cagggcgccc gaactccggg cgccgcgcc atg cgc cgg 178
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gcc agc cga gac tac ggc aag tac ctg cgc agc tcg gag gag atg ggc   226
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      5                  10                  15
agc ggc ccc ggc gtc cca cac gag ggt ccg ctg cac ccc gcg cct tct   274
Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser
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gca ccg gct ccg gcg ccg cca ccc gcc gcc tcc cgc tcc atg ttc ctg   322
Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu
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ttc ctg tac ttt cga gcg cag atg gat cct aac aga ata tca gaa gac   418
Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp
            70                  75                  80
agc act cac tgc ttt tat aga atc ctg aga ctc cat gaa aac gca ggt   466
Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly
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ttg cag gac tcg act ctg gag agt gaa gac aca cta cct gac tcc tgc   514
Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys
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agg agg atg aaa caa gcc ttt cag ggg gcc gtg cag aag gaa ctg caa   562
Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln
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cac att gtg ggg cca cag cgc ttc tca gga gct cca gct atg atg gaa   610
His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu
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Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro
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aaa gtc act ctg tcc tct tgg tac cac gat cga ggc tgg gcc aag atc   754
Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile
180                 185                 190                 195
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Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly
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Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser
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gga agc gta cct aca gac tat ctt cag ctg atg gtg tat gtc gtt aaa   898
Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys
        230                 235                 240
acc agc atc aaa atc cca agt tct cat aac ctg atg aaa gga ggg agc   946
Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser
    245                 250                 255
acg aaa aac tgg tcg ggc aat tct gaa ttc cac ttt tat tcc ata aat   994
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Gly Ala Phe Lys Val Gln Asp Ile Asp
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35 40 45
Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
50 55 60
Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
65 70 75 80
Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
85 90 95
Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
100 105 110
Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
115 120 125
Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
130 135 140
Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
145 150 155 160
Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
165 170 175
Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
180 185 190
Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
195 200 205
Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
210 215 220
Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
225 230 235 240
Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
245 250 255
Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
260 265 270
Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
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cac caa cac caa cat caa cat caa cat caa cat caa aaa cct gaa gct   96
His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro Glu Ala
            20                  25                  30
cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct tct ggt   144
Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly
        35                  40                  45
tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt tgg gct   192
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Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln
65                  70                  75                  80
gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat cac gaa   288
Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu
                85                  90                  95
acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt tac gtt   336
Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val
            100                 105                 110
gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg aaa ggt   384
Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly
        115                 120                 125
ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc tac tct   432
Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser
    130                 135                 140
atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa atc tct   480
Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser
145                 150                 155                 160
atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac gct acc   528
Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr
                165                 170                 175
tac ttc ggg gcc ttc aaa gtt cag gac atc gac tag                   564
Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
            180                 185
```

<210> 8
<211> 187
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR product with optimum codons for E. coli and P. pastoris expression

<400> 8
Glu Leu Gly Ser Leu Glu Lys Arg Glu Ala Glu Ala His Val Met Lys
1 5 10 15
His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro Glu Ala
20 25 30
Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly
35 40 45
Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala
50 55 60
Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln
65 70 75 80
Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu
85 90 95
Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val
100 105 110
Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly
115 120 125
Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser
130 135 140
Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser
145 150 155 160
Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr
165 170 175
Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
180 185

<210> 9
<211> 519
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DNA encoding murine OPGL, residues 158-316, fused to His tag

<220>
<221> CDS
<222> (1)..(519)

<220>
<221> misc_binding
<222> (1)..(42)
<223> His tag

<220>
<221> misc_feature
<222> (43)..(519)
<223> Murine OPGL, residues 158-316

<400> 9

```
atg aaa cac caa cac caa cat caa cat caa cat caa cat caa aaa cct   48
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
  1               5                  10                  15
gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct   96
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
            20                  25                  30
tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt   144
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
        35                  40                  45
tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt   192
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
    50                  55                  60
aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat   240
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
65                  70                  75                  80
cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt   288
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
                85                  90                  95
tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg   336
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
            100                 105                 110
aaa ggt ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc   384
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
        115                 120                 125
tac tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa   432
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
    130                 135                 140
atc tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac   480
Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
145                 150                 155                 160
gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac               519
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
                165                 170
```

<210> 10
<211> 173
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DNA encoding
murine OPGL, residues 158-316, fused to His tag

<400> 10

```
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
  1               5                  10                  15
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
            20                  25                  30
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
        35                  40                  45
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
    50                  55                  60
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
65                  70                  75                  80
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
                85                  90                  95
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
            100                 105                 110
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
        115                 120                 125
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
```

```
    130                 135                 140
Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
145                 150                 155                 160
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
                165                 170
```

<210> 11
<211> 519
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion of murine OPGL, residues 158-316 with C to S mutation, and His tag

<220>
<221> CDS
<222> (1)..(519)

<220>
<221> misc_binding
<222> (1)..(42)
<223> His tag

<220>
<221> misc_feature
<222> (43)..(228)
<223> Murine OPGL, residues 158-219

<220>
<221> misc_feature
<222> (232)..(519)
<223> Murine OPGL, residues 221-316

<220>
<221> mutation
<222> (229)..(231)
<223> tgt (Cys) to tcc (Ser)

<220>

<400> 11

```
atg aaa cac caa cac caa cat caa cat caa cat caa cat caa aaa cct   48
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
  1               5                  10                  15
gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct   96
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
            20                  25                  30
tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt   144
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
        35                  40                  45
tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt   192
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
    50                  55                  60
aac cag gac ggt ttc tac tac ctg tac gct aac atc tcc ttc aga cat   240
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Ser Phe Arg His
65                  70                  75                  80
cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt   288
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
                85                  90                  95
```

```
tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg   336
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
            100                 105                 110
aaa ggt ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc   384
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
        115                 120                 125
tac tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa   432
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
    130                 135                 140
atc tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac   480
Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
145                 150                 155                 160
gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac               519
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
                165                 170
```

<210> 12
<211> 173
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion of murine OPGL, residues 158-316 with C to S mutation, and His tag

<400> 12

```
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
  1               5                  10                  15
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
            20                  25                  30
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
        35                  40                  45
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
    50                  55                  60
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Ser Phe Arg His
65                  70                  75                  80
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
                85                  90                  95
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
            100                 105                 110
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
        115                 120                 125
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
    130                 135                 140
Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
145                 150                 155                 160
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
                165                 170
```

<210> 13
<211> 564
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion of murine OPGL, residues 158-316 modified by introduction of tetanus toxoid P30 epitope, and His tag

<220>
<221> CDS
<222> (1)..(564)

<220>
<221> misc_binding
<222> (1)..(42)
<223> His tag

<220>
<221> misc_feature
<222> (43)..(336)
<223> Murine OPGL, residues 158-255

<220>
<221> misc_feature
<222> (337)..(399)
<223> Tetanus toxoid P30 epitope

<220>
<221> misc_feature
<222> (400)..(564)
<223> Murine OPGL, residues 262-316

<400> 13

```
atg aaa cac caa cac caa cat caa cat caa cat caa cat caa aaa cct   48
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
  1               5                  10                  15
gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct   96
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
            20                  25                  30
tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt   144
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
        35                  40                  45
tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt   192
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
    50                  55                  60
aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat   240
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
65                  70                  75                  80
cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt   288
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
                85                  90                  95
tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg   336
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
            100                 105                 110
ttc aac aac ttc acc gtt tct ttc tgg ctg agg gta ccg aaa gtt tct   384
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
        115                 120                 125
gct tct cac ctg gaa aac tgg tct ggt aac tct gaa ttc cat ttc tac   432
Ala Ser His Leu Glu Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
    130                 135                 140
tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa atc   480
Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
145                 150                 155                 160
tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac gct   528
Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
                165                 170                 175
acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac                   564
Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
            180                 185
```

<210> 14
<211> 188
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion of murine OPGL, residues 158-316 modified by introduction of tetanus toxoid P30 epitope, and His tag

<400> 14
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
1 5 10 15
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
20 25 30
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
35 40 45
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
50 55 60
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
65 70 75 80
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
85 90 95
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
100 105 110
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
115 120 125
Ala Ser His Leu Glu Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
130 135 140
Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
145 150 155 160
Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
165 170 175
Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
180 185

<210> 15
<211> 546
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion between murine OPGL, residues 158-316 with tetanus toxoid P2 epitope introduced, and His tag

<220>
<221> CDS
<222> (1)..(546)

<220>
<221> misc_binding
<222> (1)..(42)
<223> His tag

<220>
<221> misc_feature
<222> (43)..(336)
<223> Murine OPGL, residues 158-255

<220>
<221> misc_feature
<222> (382)..(546)
<223> Murine OPGL, residues 262-316

<220>
<221> misc_feature
<222> (337)..(381)
<223> Tetanus toxoid P2 epitope

<400> 15
atg aaa cac caa cac caa cat caa cat caa cat caa cat caa aaa cct 48
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
 1   5   10   15
gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct 96
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
            20   25   30
tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt 144
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
        35   40   45
tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt 192
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
    50   55   60
aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat 240
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
65   70   75   80
cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt 288
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
                85   90   95
tac gtt gtt aaa acc cct atc aaa atc caa tct tca cat aac ctg atg 336
Tyr Val Val Lys Thr Pro Ile Lys Ile Gln Ser Ser His Asn Leu Met
            100   105   110
cag tac atc aaa gct aat tcg aaa ttc atc ggt atc acc gaa ctg aac 384
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asn
        115   120   125
tgg tct ggt aac tct gaa ttc cat ttc tac tct atc aac gtt ggt ggt 432
Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly
    130   135   140
ttc ttc aaa ctg aga gct ggt gaa gaa atc tct atc cag gtt tct aac 480
Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn
145   150   155   160
cct tct ctg ctg gac cca gac cag gac gct acc tac ttc ggg gcc ttc 528
Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe
                165   170   175
aaa gtt cag gac atc gac 546
Lys Val Gln Asp Ile Asp
            180

<210> 16
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion
      between murine OPGL, residues 158-316 with tetanus
      toxoid P2 epitope introduced, and His tag

<400> 16
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
 1   5   10   15

```
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
            20                  25                  30
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
        35                  40                  45
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
    50                  55                  60
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
65                  70                  75                  80
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
                85                  90                  95
Tyr Val Val Lys Thr Pro Ile Lys Ile Gln Ser Ser His Asn Leu Met
            100                 105                 110
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asn
        115                 120                 125
Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly
    130                 135                 140
Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn
145                 150                 155                 160
Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe
                165                 170                 175
Lys Val Gln Asp Ile Asp
            180
```

<210> 17
<211> 519
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion between murine OPGL, residues 158-316 with tetanus toxoid P2 epitope introduced, and His tag

<220>
<221> CDS
<222> (1)..(519)

<220>
<221> misc_binding
<222> (1)..(42)
<223> His tag

<220>
<221> misc_feature
<222> (43)..(432)
<223> Murine OPGL, residues 158-287

<220>
<221> misc_feature
<222> (478)..(519)
<223> Murine OPGL, residues 303-316

<220>
<221> misc_feature
<222> (433)..(477)
<223> Tetanus toxoid P2 epitope

<400> 17

```
atg aaa cac caa cac caa cat caa cat caa cat caa cat caa aaa cct   48
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
  1               5                  10                  15
```

```
gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct   96
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
            20                  25                  30
tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt   144
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
        35                  40                  45
tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt   192
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
    50                  55                  60
aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aga cat   240
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
65                  70                  75                  80
cac gaa acc tct ggt tct gtt cca acc gac tac ctg cag ctg atg gtt   288
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
                85                  90                  95
tac gtt gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg   336
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
            100                 105                 110
aaa ggt ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc   384
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
        115                 120                 125
tac tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa   432
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
    130                 135                 140
cag tac atc aaa gct aat tcg aaa ttc atc ggt atc acc gaa ctg gac   480
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asp
145                 150                 155                 160
gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac               519
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
                165                 170
```

<210> 18
<211> 173
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion between
murine OPGL, residues 158-316 with tetanus toxoid
P2 epitope introduced, and His tag

<400> 18

```
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
  1               5                  10                  15
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
            20                  25                  30
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
        35                  40                  45
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
    50                  55                  60
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
65                  70                  75                  80
His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val
                85                  90                  95
Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
            100                 105                 110
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
        115                 120                 125
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
    130                 135                 140
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Asp
145                 150                 155                 160
```

Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
165 170

<210> 19
<211> 519
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion between murine OPGL, residues 158-316 with tetanus toxoid P30 epitope introduced, and His tag

<220>
<221> CDS
<222> (1)..(519)

<220>
<221> misc_binding
<222> (1)..(42)
<223> His tag

<220>
<221> misc_feature
<222> (43)..(231)
<223> Murine OPGL, residues 158-220

<220>
<221> misc_feature
<222> (295)..(519)
<223> Murine OPGL, residues 242-316

<220>
<221> misc_feature
<222> (232)..(294)
<223> Tetanus toxoid P30 epitope

<400> 19

```
atg aaa cac caa cac caa cat caa cat caa cat caa cat caa aaa cct   48
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
  1               5                  10                  15
gaa gct cag cca ttc gct cat ctg acc atc aac gct gca tcg atc cct   96
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
            20                  25                  30
tct ggt tct cat aaa gtt acc ctg tct tct tgg tat cac gac cgc ggt   144
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
        35                  40                  45
tgg gct aaa atc tct aac atg acc ctg tct aac ggt aaa ctg aga gtt   192
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
    50                  55                  60
aac cag gac ggt ttc tac tac ctg tac gct aac atc tgt ttc aac aac   240
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Asn Asn
65                  70                  75                  80
ttc acc gtt tct ttc tgg ctg agg gta ccg aaa gtt tct gct tct cac   288
Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His
                85                  90                  95
ctg gaa gtt aaa acc tct atc aaa atc cca tct tca cat aac ctg atg   336
Leu Glu Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
            100                 105                 110
aaa ggt ggt tct acc aaa aac tgg tct ggt aac tct gaa ttc cat ttc   384
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
```

```
        115                 120                 125
tac tct atc aac gtt ggt ggt ttc ttc aaa ctg aga gct ggt gaa gaa   432
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
    130                 135                 140
atc tct atc cag gtt tct aac cct tct ctg ctg gac cca gac cag gac   480
Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
145                 150                 155                 160
gct acc tac ttc ggg gcc ttc aaa gtt cag gac atc gac               519
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
                165                 170
```

<210> 20
<211> 173
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion between murine OPGL, residues 158-316 with tetanus toxoid P30 epitope introduced, and His tag

<400> 20

```
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln Lys Pro
  1               5                  10                  15
Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro
            20                  25                  30
Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly
        35                  40                  45
Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val
    50                  55                  60
Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Asn Asn
65                  70                  75                  80
Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser Ala Ser His
                85                  90                  95
Leu Glu Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met
            100                 105                 110
Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe
        115                 120                 125
Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu
    130                 135                 140
Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
145                 150                 155                 160
Ala Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
                165                 170
```

<210> 21
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 21

```
agctgcaggt agtcggttgg aacagaacca gaggtttcgt gatgtctgaa acagatgtta 60
gcgtacag                                                          68
```

<210> 22

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 22
ctcatctgac catcaacgct gcat 24

<210> 23
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 23
tttcggtacc ctcagccaga aagaaacggt gaagttgttg aaacagatgt tagcgtacag 60
gtag 64

<210> 24
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 24
tgagggtacc gaaagtttct gcttctcacc tggaagttaa aacccctatc aaaatccaat 60
c 61

<210> 25
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 25
tttcggtacc ctcagccaga aagaaacggt gaagttgttg aacatcaggt tatgtgaaga 60
ttg 63

<210> 26
<211> 62
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 26
tgagggtacc gaaagtttct gcttctcacc tggaaaactg gtctggtaac tctgaattcc 60
at 62

<210> 27
<211> 79
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 27
tacctgcagc tgatggttta cgttgttaaa acccctatca aaatccaatc ttcacataac 60
ctgatgcagt acatcaaag 79

<210> 28
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 28
tggaattcag agttaccaga ccagttcagt tcggtgatac cgatgaattt cgaattagct 60
ttgatgtact gcatcaggtt atg 83

<210> 29
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 29
gaatttcgaa ttagctttga tgtactgttc ttcaccagct ctcagtttg 49

<210> 30
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 30
gctaattcga aattcatcgg tatcaccgaa ctggacgcta cctacttcgg ggc 53

<210> 31
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 31
cttactagtc gatgtcctga actttg 26

<210> 32
<211> 74
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic PCR primer

<400> 32
agtggaattc agagttacca gaccagtttt tggtagaacc acctttcatc aggttatgtg 60
aagatgggat tttg 74

<210> 33
<211> 65
<212> DNA
<213> Clostridium tetani

<400> 33
actacctgca gctgatggtt tacgttgtta aaacctctat caaaatccca tcttcacata 60
acctg 65

<210> 34
<211> 15
<212> PRT
<213> Clostridium tetani

<400> 34
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu
1 5 10 15

<210> 35
<211> 21
<212> PRT
<213> Clostridium tetani

<400> 35
Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
1 5 10 15
Ala Ser His Leu Glu
20

<210> 36
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Pan DR Epitope (PADRE) Peptide

<400> 36

Ala Lys Phe Val Ala Ala Trp Thr Leu Lys Ala Ala Ala
1 5 10